

#5



1/3

09900497.123456

CTGCAGTCTATTGGATGAAGAGTGTACATATTCATATAATTCTTAAAGTAGGCAGAAATTAAAG
GGGATGGAAATATATACTTGTACTGCCTTAGATAGTCACCAGGATGTTGTTACAGTCTTCGTTT
ACTGCTTCTGAAGCCTATACTGATAGAATTAATAAAATACTGAGAGAGAGAGAGAGGGACAGAG
AGAGAGAGGGGGAAGA
GAAGAAAACAAGGTSAGCCATCTGCTTAACCTTATGTCCACATTCTCTCAAGAGCATTTGTCCTA
TTTGTAGAATTATCTATATTGTTAAGAATCATCTCCATTGTTAAGATTTTGTGGGCTGGAGATC
CAGCTCTGTTGATAAAGTGCTTGCCTAACATGCATGAAGTCCTAGGTTCTATTCCCAAGGCTAC
ATAAAACCTTGTGTTGTGATGAATGCCTGTAATCCCAGTACGCAGCAAGGAGAGACAAGGAGGA
TCAGAAAGCTTAAGGACATCATTTTGTACATAGTGAGTTTGAGGAAAGCTGAGGTTACATGGAAC
TCTCTCTCTCTCAAAAACAAAACAAAACAAAACCTTCTACTAATATTCTGGATTCTGTT
TGATTTTTAGGATCTCAAGAGCATGCTGACGTCATTTATGTGTTTCCATCAGATACAGACAGAG
ATCATAAACATTTAACTCATTTGATTATATGTTGAGAGTTGTCCCTCAAGAACCAATGGCCAAAC
ATCCACTGAGGATACACGGAAGCTTAGAAAATCTCTAATTAATAATCCTGACATAATGGAAGTGC
TCACAAACCAGCCAACACCTAATAAAACCAGTGGCAAGAGCAACAACCTCGGCATTTTTCTACTT
TGAATCCTGCCAACCCCTTTTCTAGCCATACTCTTGCTACTCATAGCATATACTGTGATCCTA
ATCATGGGCATTTTTTGAAACCTCTCTCTTATCATCATCATCTTTAAGAAACAGAGAGAAGCTC
AAAATGTTACCAACATACTGATTGCCAACCTGTCCCTCTCTGACATCTTGGTGTGTGTCATGTG
CATCCCTTTTACGGTCATCTACACTCTGATGGACCACTGGGTATTTGGGAACACTATGTGTAA
CTCACTTCTTACGTGCAAAGTGTCTCAGTTTCTGTGTCCATATTCTCCCTTGTGTTGATTGCTA
TTGAACGATATCAGCTGATTGTGAACCCCGTGGCTGGAAACCCAGAGTAGCTCATGCCTATTG
GGGATCATCTTGATTGGCTCATTTCTCTGACATTGTCTATTCCCTTATTCCCTGTCTTACCAC
CTCACCAATGAGCCCTTTCATAATCTCTCTCTCCCTACTGACATCTACACCCACCAGGTAGCTT
GTGTGGAGATTTGGCCTTCTAACTGAACCAACTCCTCTTTTCTACATCATTTATTTATGCTCCA
GTATTTTGTCCCTCTGGGTTTCACTTCTTATCTGCTACCTGAAGATCGTTCTCTGCCTCCGAAAA
AGAACTAGGCAGGTGGACAGGAGAAAGGAAAATAAGAGCCGTCTCAATGAGAACAAGAGGGTAA
ATGTGATGTTGATTTCATCGTAGTGACTTTTGGAGCCTGCTGGTTGCCCTTGAACATTTTCAA
TGTCATCTTCGACTGGTATCATGAGATGCTGATGAGCTGCCACCACGACCTGGTATTTGTAGTT
TGCCACTTGATTGCTATGGTTTCTACTTGCATAAATCCTCTCTTTTATGGATTTCTCAACAAAA
ACTTCCAGAAGGATCTAATGATGCTTATTCACCACTGTTGGTGTGGTGAACCTCAGGAAAGTTA
TGAAAATATTGCCATGTCTACTATGCACACAGATGAATCCAAGGGATCATTAAACTGGCTCAC
ATACCAACAGGCATATAGAACTGGTAAGCAAAATCAAAGCCCTTCTGTTATGAAAGAAAGAGA
AGAAATAGTATGGAATAGGGCAAGGTGCAGAGGAAGCCAGACTTAAACACATAATATCTTTGGG
CCAGTTTTGCTTTAAGTTAAGCATGTCTACTCCATTAGCCATAGAACACACAGAGATTTATC
CCTACCCTTTCTTTTTTTTCTTTTGAAGAATAATAACTTAAACAACCTAGACATCATTAAGGAG
GAAGAGAACAAAATGAGAGAGCATACAAGGACAGCAGAGATGTCTGGGGTACAAAATTCACGT
TATTCGCTGGAATAGCTAGAAAGTTATTAGTTGTGCTGCAG (SEQ ID NO:1)

FIGURE 1

underlined = deleted in targeting construct

[] = sequence flanking Neo insert in targeting construct

[CTGCAGTCTATTGGATGAAGAGTGTACATATTCATATAATTCTTAAAGTAGGCAGAAAT
 TAAAGGGGATGGAAATATATACTTGTACTGCCTTAGATAGTCACCAGGATGTTGTTACAG
 TCTTCGTTTACTGCTTCTGAAGCCTATACTGATAGAATTAATAAAATACTGAGAGAGAGA
 GAGAGGGACAGAGAGAGAGAGAGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
 GAGAGAGAGAGAGAAGAGAAGAAAACAAGGTSAAAGCCATCTGCTTAACCTTATGTCCACAT
 TCTCTCAAGAGCATTGTCTTATTTGTAGAATTATCTATATTGTTAAGAATCATCTCCATT
 GTTAAGATTTTGTGGGCTGGAGATCCAGCTCTGTTGATAAAGTGCTTGCCTAACATGCAT
 GAAGTCCTAGGTTCTATTCCCAAGGCTACATAAAACCTTGTGTTGTGATGAATGCCTGTA
 ATCCCAGTACGCAGCAAGGAGAGACAAGGAGGATCAGAAGCTTAAGGACATCATTTTGTA
 CATAGTGAGTTTGAAGAAAGCTGAGGTTACATGGAACCTCTCTCTCTCAAAAACAAAAC
 AAAACAAAACAAAACCTTCTACTAATATTCTGGATTCTGTTTGATT'TTAGGATCTCAAG
 AGCATGCTGACGTCATTTATGTGTTTCCATCAGATACAGACAGAGATCATAAACATTTAA
 CTCATTGATTATATGTTGAGAGTTGTCCCTCAAGAACCAATGGCCAAACATCCACTGAGG
 ATACACGGAAGCTTAGAAAATCTCTAATTAATAATCCTGACATAATGGAAGTGCTCACAAA
 CCAGCC] AACACCTAATAAAACCAGTGGCAAGAGCAACAACCTCGGCATTTTCTACTTTG
AATCCTGCCAACCCTTTTCTAGCCATACTCTTGCTACTCATAGCATATACTGTGATCC
TAATCATGGGCATTTTGGAAACCTCTCTCTTATCATCATCATCTTTAAGAAACAGAGAG
AAGCTCAAAATGTTACCAACATACTGATT [GCCAACCTGTCCCTCTCTGACATCTTGGTG
 TGTGTCATGTGCATCCCTTTTACGGTCATCTACACTCTGATGGACCAC'TGGGTATTTGGG
 AACACTATGTGTAAACTCACTTCCCTACGTGCAAGTGTCTCAGTTTCTGTGTCCATATTC
 TCCCTTGTGTTGATTGCTATTGAACGATATCAGCTGATTGTGAACCCCGTGGCTGGAAA
 CCCAGAGTAGCTCATGCCTATTGGGGGATCATCTTGATT'TGGCTCAT'TTCTCTGACATTG
 TCTATTCCCTTATTCCTGTCTTACCACCTCACCAATGAGCCCTTTCATAATCTCTCTCTC
 CCTACTGACATCTACACCCACCAGGTAGCTTGTGTGGAGATTTGGCCTTCTAAACTGAAC
 CAATCCTCTTTTCTACATCATTATTTATGCTCCAGTATTTTGTCCCTCTGGGTTTCATT
 CTTATCTGCTACCTGAAGATCGTTCTCTGCCTCCGAAAAAGAAGTAGGCAGGTGGACAGG
 AGAAAGGAAAAATAAGAGCCGTCTCAATGAGAACAGAGGGTAAATGTGATGTTGATTTC
 ATCGTAGTGACTTTTGGAGCCTGCTGGTTGCCCTTGAACATTTTCAATGTCATCTTCGAC
 TGGTATCATGAGATGCTGATGAGCTGCCACCACGACCTGGTATTTGTAGTTTGGCACTTG
 ATTGCTATGGTTTCTACTTGCATAAATCCTCTCTTTTATGGATTTCTCAACAAAACTTC
 CAGAAG] GATCTAATGATGCTTATTCACCACTGTTGGTGTGGTGAACCTCAGGAAAGTTA
 TGAAAATATTGCCATGTCTACTATGCACACAGATGAATCCAAGGGATCATTAACACTGGC
 TCACATACCAACAGGCATATAGAACTGGTAAGCAAAATCAAAGCCCTTCTGTTATGAAA
 GAAAGAGAAGAAATAGTATGGAATAGGGCAAGGTGCAGAGGAAGCCAGACTTAAACACAT
 AATATCTTTGGGCCAGTTTGTCTTAAAGTTAAGCATGTCTACTCCATTCAGCCATAGAA
 CACACAGAGATTTATCCCTACCCTTTCTTTTTTCTTTTGAAGAATAATAACTTAAACA
 ACCTAGACATCATTTACTGAGGAAGAGAACAATAATGAGAGAGCATACAAGGACAGCAGAG
 ATGTCTGGGGTACAAAATTCACGTTATTCGCTGGAATAGCTAGAAAGTTATTAGTTGTGC
 TGCAG

FIGURE 2A

Gene Sequence Structure

*

846 bp

Sequence Deleted

1047 bp

Size of CDS: 2281 bp

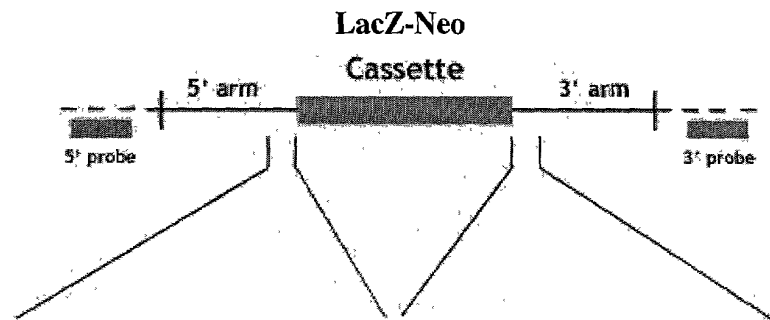
Targeting Vector*
(genomic sequence)

Construct Number: 2762

Arm Length:

5': 5 kb

3': 0.5 kb



— Targeting Vector
 - - - - Endogenous Locus

* Not drawn to scale

5' >TTTAGGATCTCAAGAGCATGC
 TGACGTCATTTATGTGTTTCCATC
 AGATACTGACAGAGATCATAAACA
 TTTAACTCATTGATTATATGTTGA
 GAGTTGTCCCTCAAGAACCAATGG
 CCAAACATCCACTGAGGATACACG
 GAAGCTTAGAAAAATCTCTAATTAA
 AATCCTGACATAATGGAAGTGCTC
 ACAAACCAGCC<3'
 (SEQ ID NO:2)

5' >GCCAACCTGTCCCTCTCTGAC
 ATCTTGGTGTGTGTCATGTGCATC
 CCTTTACGGTCATCTACACTCTG
 ATGGACCACTGGGTATTTGGAAC
 ACTATGTGTAACTCACTTCCTAC
 GTGCAAAGTGTCTCAGTTTCTGTG
 TCCATATTCTCCCTTGTGTTGATT
 GCTATTGAACGATATCAGCTGATT
 GTGAACCCCG<3'
 (SEQ ID NO:3)

FIGURE 2B